



#5

1

## SEQUENCE LISTING

COPY

&lt;110&gt; CIHLAR, TOMAS

&lt;120&gt; NOVEL GENE ENCODING ORGANIC ANION TRANSPORTER

&lt;130&gt; 240.1PCD

&lt;140&gt; 10/086,816

&lt;141&gt; 2002-02-28

&lt;150&gt; 09/330,245

&lt;151&gt; 1999-06-10

&lt;150&gt; 60/132,267

&lt;151&gt; 1999-05-03

&lt;150&gt; 60/088,864

&lt;151&gt; 1998-06-11

&lt;160&gt; 10

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 2123

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (263)..(1912)

&lt;400&gt; 1

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ggactcagct cccgggaagc aaccagctg cggaggcaac ggcagtgtg ctctccagc 180

gaaggacagc aggcaggcag acagacagag gtcctgggac tggaaggcct cagccccag 240

ccactgggct gggcctggcc ca atg gcc ttt aat gac ctc ctg cag cag gtg 292

Met Ala Phe Asn Asp Leu Leu Gln Gln Val

1

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Gly Gly Val Gly Arg Phe Gln Gln Ile Gln Val Thr Leu Val Val Leu

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ccc ctg ctc ctg atg gct tct cac aac acc ctg cag aac ttc act gct 388

Pro Leu Leu Leu Met Ala Ser His Asn Thr Leu Gln Asn Phe Thr Ala

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gcc atc cct acc cac cac tgc cgc ccg cct gcc gat gcc aac ctc agc 436

Ala Ile Pro Thr His His Cys Arg Pro Pro Ala Asp Ala Asn Leu Ser

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50

55

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Lys Asn Gly Gly Leu Glu Val Trp Leu Pro Arg Asp Arg Gln Gly Gln	
60 65 70	
cct gag tcc tgc ctc cgc ttc acc tcc ccg cag tgg gga ctg ccc ttt	532
Pro Glu Ser Cys Leu Arg Phe Thr Ser Pro Gln Trp Gly Leu Pro Phe	
75 80 85 90	
ctc aat ggc aca gaa gcc aat ggc aca ggg gcc aca gag ccc tgc acc	580
Leu Asn Gly Thr Glu Ala Asn Gly Thr Gly Ala Thr Glu Pro Cys Thr	
95 100 105	
gat ggc tgg atc tat gac aac agc acc ttc cca tct acc atc gtg act	628
Asp Gly Trp Ile Tyr Asp Asn Ser Thr Phe Pro Ser Thr Ile Val Thr	
110 115 120	
gag tgg gac ctt gtg tgc tct cac agg gcc cta cgc cag ctg gcc cag	676
Glu Trp Asp Leu Val Cys Ser His Arg Ala Leu Arg Gln Leu Ala Gln	
125 130 135	
tcc ttg tac atg gtg ggg gtg ctg ctc gga gcc atg gtg ttc ggc tac	724
Ser Leu Tyr Met Val Gly Val Leu Leu Gly Ala Met Val Phe Gly Tyr	
140 145 150	
ctt gca gac agg cta ggc cgc cgg aag gta ctc atc ttg aac tac ctg	772
Leu Ala Asp Arg Leu Gly Arg Arg Lys Val Leu Ile Leu Asn Tyr Leu	
155 160 165 170	
cag aca gct gtg tca ggg acc tgc gca gcc ttc gca ccc aac ttc ccc	820
Gln Thr Ala Val Ser Gly Thr Cys Ala Ala Phe Ala Pro Asn Phe Pro	
175 180 185	
atc tac tgc gcc ttc cgg ctc ctc tcg ggc atg gct ctg gct ggc atc	868
Ile Tyr Cys Ala Phe Arg Leu Leu Ser Gly Met Ala Leu Ala Gly Ile	
190 195 200	
tcc ctc aac tgc atg aca ctg aat gtg gag tgg atg ccc att cac aca	916
Ser Leu Asn Cys Met Thr Leu Asn Val Glu Trp Met Pro Ile His Thr	
205 210 215	
cgg gcc tgc gtg ggc acc ttg att ggc tat gtc tac agc ctg ggc cag	964
Arg Ala Cys Val Gly Thr Leu Ile Gly Tyr Val Tyr Ser Leu Gly Gln	
220 225 230	
ttc ctc ctg gct ggt gtg gcc tac gct gtg ccc cac tgg cgc cac ctg	1012
Phe Leu Leu Ala Gly Val Ala Tyr Ala Val Pro His Trp Arg His Leu	
235 240 245 250	
cag cta ctg gtc tot gcg cct ttt ttt gcc ttc ttc atc tac tcc tgg	1060
Gln Leu Leu Val Ser Ala Pro Phe Phe Ala Phe Phe Ile Tyr Ser Trp	
255 260 265	
ttc ttc att gag tcg gcc cgc tgg cac tcc tcc tcc ggg agg ctg gac	1108
Phe Phe Ile Glu Ser Ala Arg Trp His Ser Ser Ser Gly Arg Leu Asp	
270 275 280	

ctc acc ctg agg gcc ctg cag aga gtc gcc cgg atc aat ggg aag cgg	1156
Leu Thr Leu Arg Ala Leu Gln Arg Val Ala Arg Ile Asn Gly Lys Arg	
285 290 295	
gaa gaa gga gcc aaa ttg agt atg gag gta ctc cgg gcc agt ctg cag	1204
Glu Glu Gly Ala Lys Leu Ser Met Glu Val Leu Arg Ala Ser Leu Gln	
300 305 310	
aag gag ctg acc atg ggc aaa ggc cag gca tcg gcc atg gag ctg ctg	1252
Lys Glu Leu Thr Met Gly Lys Gly Gln Ala Ser Ala Met Glu Leu Leu	
315 320 325 330	
cgc tgc ccc acc ctc cgc cac ctc ttc ctc tgc ctc tcc atg ctg tgg	1300
Arg Cys Pro Thr Leu Arg His Leu Phe Leu Cys Leu Ser Met Leu Trp	
335 340 345	
ttt gcc act agc ttt gca tac tat ggg ctg gtc atg gac ctg cag ggc	1348
Phe Ala Thr Ser Phe Ala Tyr Tyr Gly Leu Val Met Asp Leu Gln Gly	
350 355 360	
ttt gga gtc agc atc tac cta atc cag gtg atc ttt ggt gct gtg gac	1396
Phe Gly Val Ser Ile Tyr Leu Ile Gln Val Ile Phe Gly Ala Val Asp	
365 370 375	
ctg cct gcc aag ctt gtg ggc ttc ctt gtc atc aac tcc ctg ggt cgc	1444
Leu Pro Ala Lys Leu Val Gly Phe Leu Val Ile Asn Ser Leu Gly Arg	
380 385 390	
cgg cct gcc cag atg gct gca ctg ctg ctg gca ggc atc tgc atc ctg	1492
Arg Pro Ala Gln Met Ala Ala Leu Leu Leu Ala Gly Ile Cys Ile Leu	
395 400 405 410	
ctc aat ggg gtg ata ccc cag gac cag tcc att gtc cga acc tct ctt	1540
Leu Asn Gly Val Ile Pro Gln Asp Gln Ser Ile Val Arg Thr Ser Leu	
415 420 425	
gct gtg ctg ggg aag ggt tgt ctg gct gcc tcc ttc aac tgc atc ttc	1588
Ala Val Leu Gly Lys Gly Cys Leu Ala Ala Ser Phe Asn Cys Ile Phe	
430 435 440	
ctg tat act ggg gaa ctg tat ccc aca atg atc cgg cag aca ggc atg	1636
Leu Tyr Thr Gly Glu Leu Tyr Pro Thr Met Ile Arg Gln Thr Gly Met	
445 450 455	
gga atg ggc agc acc atg gcc cga gtg ggc agc atc gtg agc cca ctg	1684
Gly Met Gly Ser Thr Met Ala Arg Val Gly Ser Ile Val Ser Pro Leu	
460 465 470	
gtg agc atg act gcc gag ctc tac ccc tcc atg cct ctc ttc atc tac	1732
Val Ser Met Thr Ala Glu Leu Tyr Pro Ser Met Pro Leu Phe Ile Tyr	
475 480 485 490	
ggg gct gtt cct gtg gcc gcc agc gct gtc act gtc ctc ctg cca gag	1780
Gly Ala Val Pro Val Ala Ala Ser Ala Val Thr Val Leu Leu Pro Glu	
495 500 505	

acc ctg ggc cag cca ctg cca gac acg gtg cag gac ctg gag agc agg 1828  
 Thr Leu Gly Gln Pro Leu Pro Asp Thr Val Gln Asp Leu Glu Ser Arg  
                   510                  515                  520

aaa ggg aaa cag acg cga cag caa caa gag cac cag aag tat atg gtc 1876  
 Lys Gly Lys Gln Thr Arg Gln Gln Gln Glu His Gln Lys Tyr Met Val  
                   525                  530                  535

cca ctg cag gcc tca gca caa gag aag aat gga ctc tgaggactga 1922  
 Pro Leu Gln Ala Ser Ala Gln Glu Lys Asn Gly Leu  
                   540                  545                  550

gaaggggcct tacagaaccc taaagggagg gaaggtccta caggtctccg gccacccaca 1982

caaggaggag gaagaggaaa tggtagccca agtgtggggg ttgtgggttca ggaaagcatc 2042

ttcccagggg tccacctccc ttataaaacc ccaccagaac cacatcatta aaaggtttga 2102

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<213> Homo sapiens

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                   20                  25                  30

Ser His Asn Thr Leu Gln Asn Phe Thr Ala Ala Ile Pro Thr His His  
                   35                  40                  45

Cys Arg Pro Pro Ala Asp Ala Asn Leu Ser Lys Asn Gly Gly Leu Glu  
                   50                  55                  60

Val Trp Leu Pro Arg Asp Arg Gln Gly Gln Pro Glu Ser Cys Leu Arg  
                   65                  70                  75                  80

Phe Thr Ser Pro Gln Trp Gly Leu Pro Phe Leu Asn Gly Thr Glu Ala  
                   85                  90                  95

Asn Gly Thr Gly Ala Thr Glu Pro Cys Thr Asp Gly Trp Ile Tyr Asp  
                   100                  105                  110

Asn Ser Thr Phe Pro Ser Thr Ile Val Thr Glu Trp Asp Leu Val Cys  
                   115                  120                  125

Ser His Arg Ala Leu Arg Gln Leu Ala Gln Ser Leu Tyr Met Val Gly  
                   130                  135                  140

Val Leu Leu Gly Ala Met Val Phe Gly Tyr Leu Ala Asp Arg Leu Gly  
                   145                  150                  155                  160

Arg Arg Lys Val Leu Ile Leu Asn Tyr Leu Gln Thr Ala Val Ser Gly  
 165 170 175  
 Thr Cys Ala Ala Phe Ala Pro Asn Phe Pro Ile Tyr Cys Ala Phe Arg  
 180 185 190  
 Leu Leu Ser Gly Met Ala Leu Ala Gly Ile Ser Leu Asn Cys Met Thr  
 195 200 205  
 Leu Asn Val Glu Trp Met Pro Ile His Thr Arg Ala Cys Val Gly Thr  
 210 215 220  
 Leu Ile Gly Tyr Val Tyr Ser Leu Gly Gln Phe Leu Leu Ala Gly Val  
 225 230 235 240  
 Ala Tyr Ala Val Pro His Trp Arg His Leu Gln Leu Leu Val Ser Ala  
 245 250 255  
 Pro Phe Phe Ala Phe Phe Ile Tyr Ser Trp Phe Phe Ile Glu Ser Ala  
 260 265 270  
 Arg Trp His Ser Ser Ser Gly Arg Leu Asp Leu Thr Leu Arg Ala Leu  
 275 280 285  
 Gln Arg Val Ala Arg Ile Asn Gly Lys Arg Glu Glu Gly Ala Lys Leu  
 290 295 300  
 Ser Met Glu Val Leu Arg Ala Ser Leu Gln Lys Glu Leu Thr Met Gly  
 305 310 315 320  
 Lys Gly Gln Ala Ser Ala Met Glu Leu Leu Arg Cys Pro Thr Leu Arg  
 325 330 335  
 His Leu Phe Leu Cys Leu Ser Met Leu Trp Phe Ala Thr Ser Phe Ala  
 340 345 350  
 Tyr Tyr Gly Leu Val Met Asp Leu Gln Gly Phe Gly Val Ser Ile Tyr  
 355 360 365  
 Leu Ile Gln Val Ile Phe Gly Ala Val Asp Leu Pro Ala Lys Leu Val  
 370 375 380  
 Gly Phe Leu Val Ile Asn Ser Leu Gly Arg Arg Pro Ala Gln Met Ala  
 385 390 395 400  
 Ala Leu Leu Leu Ala Gly Ile Cys Ile Leu Leu Asn Gly Val Ile Pro  
 405 410 415  
 Gln Asp Gln Ser Ile Val Arg Thr Ser Leu Ala Val Leu Gly Lys Gly  
 420 425 430  
 Cys Leu Ala Ala Ser Phe Asn Cys Ile Phe Leu Tyr Thr Gly Glu Leu  
 435 440 445  
 Tyr Pro Thr Met Ile Arg Gln Thr Gly Met Gly Met Gly Ser Thr Met  
 450 455 460

Ala Arg Val Gly Ser Ile Val Ser Pro Leu Val Ser Met Thr Ala Glu  
465 470 475 480

Leu Tyr Pro Ser Met Pro Leu Phe Ile Tyr Gly Ala Val Pro Val Ala  
485 490 495

Ala Ser Ala Val Thr Val Leu Leu Pro Glu Thr Leu Gly Gln Pro Leu  
500 505 510

Pro Asp Thr Val Gln Asp Leu Glu Ser Arg Lys Gly Lys Gln Thr Arg  
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Gln Glu Lys Asn Gly Leu  
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tgacctctg cagcagg 77

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<220>  
<223> Description of Artificial Sequence: Synthetic  
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<400> 8  
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<210> 9  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

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<210> 10  
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
immunogenic peptide

<400> 10

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